93.2% and 91.5%. The QFT had 58.3% sensitivity and 95.3% specificity in diagnosing children with latent TB. The commonest discordant results were TST+/ QFT- in 15 of 141 children without TB, not unexpected in this BCG-vaccinated population.

Conclusion: The QFT performed better than the TST in the diagnosis of tuberculosis. Although only moderately sensitive, they were highly specific in ruling out TB and showed good concordance in TB-negative children. Although a case may be made for using both tests in BCG-vaccinated children, the higher costs and technical expertise required for the QFT do not support its use instead of the cheaper and simpler TST in India.

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Accuracy of the Xpert MTB/RIF assay compared to the "gold standard" AFB culture in the diagnosis of tuberculosis in children in India

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Background: The Xpert MTB/RIF PCR assay detects *M.tuberculosis* and resistance to Rifampicin within 2-4 hours, compared to the AFB culture that takes 4-8 weeks to provide the same information. This study assessed the performance of the Xpert MTB/RIF assay against the AFB culture and clinical case definitions of intrathoracic and extrathoracic tuberculosis(TB), and against type of specimen tested.

Methods & Materials: All children < 16 years of age with suspected TB seen in the Pediatric Department, Christian Medical College, Vellore from May 2012-June 2015 and tested with Xpert MTB/RIF assay and AFB cultures in the Department of Clinical Microbiology were included. Records and test results were accessed to classify children as confirmed, probable or possible TB or TB unlikely/not TB based on the 2014 NIH/WHO consensus and other case definitions.

Results: 286 children with suspected TB (135 intrathoracic, 71 lymphadenitis, 51 meningitis and 28 abdominal) were reviewed. 41 of 52 children with culture-confirmed TB had a positive Xpert MTB/RIF assay (overall sensitivity 78.9%). 115 more children were case-defined TB, while 119 had no TB.

The sensitivity of the Xpert MTB/RIF assay against the AFB culture was 96% in intrathoracic TB, 78% for TB lymphadenitis, 67% for TB abdomen and 46% for TB meningitis. The assay showed less sensitivity against clinical case definitions, being 48% for intrathoracic TB, 47% for TB lymphadenitis, 41% for TB abdomen and 19% for TB meningitis. The assay diagnosed an additional 15 children with intrathoracic TB, 11 children with TB lymphadenitis, and 3 and 2 children with TB abdomen and TB meningitis compared to the AFB culture. Sensitivity was 100% for sputum specimens, intrathoracic tissue and BAL samples, 90% for gastric aspirates, 78% for lymph nodes, 67% for intra-abdominal tissue and 46% for CSF against the AFB culture. It was 80% sensitive in detecting Rifampicin resistance. The specificity of the assay in disease-negative children was 92% for intra-thoracic and abdominal TB, 93% for TB lymphadenitis, and 100% for TB meningitis.

Conclusion: The Xpert MTB/RIF assay's high sensitivity, specificity and detection of Rifampicin resistance make it a good point-of-care test for early diagnosis of childhood tuberculosis, especially intrathoracic TB.

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Population structure and molecular epidemiology of human clinical multi-drug resistant (MDR) Escherichia coli strains from Pune, India

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Background: Extraintestinal pathogenic *E. coli* (ExPEC) cause different infectious diseases in humans and animals, accounting 80% of urinary tract infections (UTIs), worldwide. Increase in the prevalence of multidrug-resistant (MDR) *E. coli* and global dissemination of these clonal organisms is a significant risk to the public health. The present study investigates the prevalence, population structure, phylogenetic affinities and molecular basis of ESBL and antimicrobial resistance and also highlights the spread of multi-drug resistant *E. coli* causing infections with varied clinical spectrum

Methods & Materials: A total of 187 *E. coli* isolates from patients with different clinical complications were obtained from D.Y. Patil Medical College, Pune, for this study. All the isolates were subjected to phylogenetic grouping and specific sequence type (ST) identification. The ST131 strains were further evaluated for their virulence gene profiles using PCR. Phenotypic and genotypic detections of antimicrobial resistance were carried out by disc diffusion and PCR based methods, respectively. The clonality of ST131 isolates with respect to strains of other sequence types was evaluated by enterobacterial repetitive intergenic consensus PCR (ERIC-PCR).

Results: Phylogrouping of 187 *E. coli* isolates revealed that 78 (41.7%) isolates belonged to group A, 16 (8.6%) to group B1, 56 (29.9%) to group B2 and 37 (19.8%) to group D. Forty strains were identified to belong to ST131. Virulence profiling of ST131 strains demonstrated significant prevalence of *fimH* (90%), *papC* (82.5%), *hlyA* (77.5%) *traT* (47.5%), *sat* (87.5%) and *iucD* (55%). The antibiotic resistance profiles of ST131 isolates showed high resistance to ciproflaxin (92.5%), cotrimoxazole (67.5%) and tetracycline (62.5%). A high proportion (60%) of these ST131 strains was multidrug resistant and 95% were ESBL-positive. Of all the 40 ST131 strains, 42.5% and 95% were positive for sulphonamide and streptomycin resis-

tance encoding genes, respectively, and only 2 strains were found to be positive for *ndm-1*.

Conclusion: Our study revealed that ST131 is the only predominant endemic clone present in the clinical *E. coli* isolates from Pune. Molecular characterization of these isolates suggests that ST131 is a robust lineage of pathogen that could significantly limit medical interventions against *E. coli* induced enteric and extraintestinal infections in India.

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Antibiotic resistance among gastrointestinal and respiratory tract bacterial pathogens in Mauritius

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Background: Antibiotic resistance rates vary markedly according to geographical region. It is thus essential to have local data on antibiotic resistance to determine the choice of antibiotics for empirical treatment of bacterial infections. A survey was therefore conducted to determine antibiotic resistance rates in 2014 of the main bacterial causes of gastroenteritis and respiratory tract infections in humans, namely nontyphoidal *Salmonella, Campylobacter, Streptococcus pneumoniae* and *Haemophilus influenza*e.

Methods & Materials: Laboratory registers at the two government laboratories which perform microbiological examination were reviewed. Antibiotic susceptibility results of all nontyphoidal *Salmonella* and *Campylobacter* from stool specimens, and pneumococcus and *H.influenzae* from sputum, sinus and ear specimens were recorded. Duplicate isolates from the same patient were excluded.

Results: In 2014, 115 *Salmonella* isolates were recorded and susceptibility rates to ampicillin, co-trimoxazole, nalidixic acid and ciprofloxacin were 100%, 98%, 99% and 100% respectively. In contrast only 49% of 101 *Campylobacter* isolates were susceptible to ciprofloxacin although 96% were susceptible to erythromycin. Among respiratory tract pathogens, only 21 of 48 (44%) of pneumococcus isolates were susceptible to erythromycin and 63% had reduced sensitivity to penicillin (Minimum inhibitory concentration [MIC] $\geq$0.1 μg/mL) but none had high level penicillin resistance (MIC > 2 μg/mL). 96% and 100% of pneumococci were susceptible to tetracycline and levofloxacin respectively. 27 of 35 (77%) of *Haemophilus influenzae* isolates were susceptible to ampicillin and all were susceptible to cefotaxime, amoxicillin-clavulanic acid combination and levofloxacin.

Conclusion: High rates of resistance were observed for some organism-antibiotic combinations in Mauritius in 2014 such as for ciprofloxacin in *Campylobacter* and erythromycin in pneumococcus. When compared to historical data, resistance to ciprofloxacin in *Campylobacter* in Mauritius increased from 3.6% in 1998-2005 to 51% in 2014 and this was probbably due to antibiotic overuse in veterinary practice. In severe bacterial gastroenteritis requiring antibiotic therapy, ciprofloxacin is likely to be effective against *Salmonella* but not against *Campylobacter*. Macrolide antibiotics cannot be relied upon as monotherapy to treat infections likely to be caused by pneumococcus in Mauritius. Control of antibiotic use is required in both medical and veterinary practice to minimize the emergence and spread of antibiotic-resistant bacteria.

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Re-emergence of susceptibility to conventional first line drugs in Salmonella isolates: an old weapon to fight NARS

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Background: Enteric fever, caused by *Salmonella* is a common clinical diagnosis among febrile patients presenting to hospital in Nepal. The first-line drugs ampicillin, chloramphenicol and cotrimoxazole have not been part of empirical therapy due to development of multidrug-resistant Salmonella. Ciprofloxacin has been the empirical therapy of choice, but the recent increase in minimum inhibitory concentration (MIC) to ciprofloxacin in *Salmonella enterica*, may result in delayed response and serious complications. The current study investigates the re-emergence of sensitivity to conventionally used drugs among strains of S. Typhi and S. Paratyphi A in a community hospital of Kathmandu.

Methods & Materials: We evaluated 245 Salmonella isolates, at Helping-Hands Community Hospital, Chabahil, Kathmandu, for chloramphenicol, ampicillin and cotrimoxazole susceptibility using standard methods as per the guidelines of the Clinical and Laboratory Standards Institute .

Results: Of the total 245 positive isolates, 50.20% (123/245) were *S.* Typhi and 49.80% (122/245) were *S.* Paratyphi A. A total of 229 (93.5%) were Nalidixic Acid Resistant (NAR) *Salmonella*, including 110(89.4%) *S.* Typhi and 119(97.5%) *S.* Paratyphi A. More than 95% of the isolates were sensitive to ampicillin, chloramphenicol, cotrimoxazole, ceftriaxone, and cefixime.

Conclusion: First generation drug were found effective indicating re-emergence of susceptibility to conventional first line antimicrobial which may play important role in the treatment of NAR and non MDR *Salmonella* isolate.

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